REMARKS

Claims 1-3, 9, 14-27, and 30 are pending. Claims 16-24 and 26 have been previously withdrawn. New Claim 31 is added herein. Therefore, Claims 1-3, 9, 14-27, 30, and 31 are under consideration. Claims 1 and 30 have been amended to recite that the derivatives have at least 70% sequence identity and 80% sequence identity, respectively. New Claim 31 recites that the derivatives have at least 90% sequence identity. Support new Claim 31 and for the amendments to Claims 1 and 30 can be found throughout the specification and at least on page 10, lines 26-36, where percentage sequence identity for the derivatives can be found. Claim 14 has been amended to remove the recitation "or fragment of 4 or 5 residues….sequence homology." Applicants believe that these amendments do not raise new issues nor constitute new matter.

OBJECTIONS TO THE CLAIMS

Claims 1,14 and 30 are objected to for allegedly containing informalities. In particular, the Examiner objects to Claims 1 and 30 for the recitation "SEQ ID No." rather than "SEQ ID NO: ." Although Applicants are not aware of any rule dictating the particular format suggested by the Examiner, in an effort to further prosecution, Claims 1 and 30 have been amended herein to remove the offending recitation and replace it with the Examiner suggested format. Applicants believe the objection to be moot in light of the amendments to Claims 1 and 30 and respectfully request its withdrawal.

Regarding Claim 14, the Examiner objects to the claim for allegedly containing an amino acid sequence without a sequence identifier. Claim 14 has been amended to include recitation of a sequence identifier. Applicants believe the objection to be moot in light of this amendment and respectfully request its withdrawal.

35 U.S.C. § 112, 1ST PARAGRAPH, REJECTIONS

The Office Action rejected Claims 1-3, 9, 14, 15, 25, 27, and 30 under 35 U.S.C. § 112, 1st paragraph, as failing to comply with the written description requirement. Specifically, the Office Action stated that these claims were rejected because "the disclosure does not disclose a structure to function correlation for the genus of signal peptides having at least 60% sequence homology to SEQ ID NO: 1 or SEQ ID NO: 2 or a derivative thereof."

(Office Action, p. 3). Applicants respectfully traverse this rejection to the extent that the rejection applies to the amended claims.

Applicants respectfully remind the Examiner that the standard for written description is conveyance of the claimed subject matter "with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. *Vas-Cath Inc. v Mahurka* 935 F2d 1555 -64, 19 USPQ2d 1111, 1117 (Fed. Cir. 1991). Applicants respectfully submit that this standard has been met by the description in the specification for the Claims as presently amended. Specifically, Applicant would like to point out that the claims on which the present Official Action is based are limited to the use of a genus of signal peptides having at least 60% sequence **identity** to SEQ ID NO: 1 or SEQ ID NO: 2 **NOT homology** as asserted by the Examiner on page 3 of the present rejection.

As discussed in the paragraph bridging pages 9 and 10, sequence identity is a more stringent measure of sequence correspondence. This is because calculations of sequence homology do not treat amino acids that are interchangeable on the basis of similar physical characteristics such as charge and polarity as being different, whereas calculations of sequence identity do. Accordingly, the genus described by the claims on which the present Office Action is based is in fact not as broad as the Examiner has interpreted it to be. Nevertheless, to advance prosecution of this application claim 1 has been further limited to refer to the use of signal peptides of SEQ ID NO: 1 or SEQ ID NO: 2 or derivatives having at least **70**% sequence **identity** thereto.

As described in the application in the paragraph bridging pages 9 and 10, sequence identity is very easy to determine because the skilled man merely needs to align his two sequences of interest to ascertain if any differences exist between the residues situated at any particular position. Since SEQ ID NO: 1 and SEQ ID NO: 2 are relatively short stretches of amino acid sequence (17 and 14 amino acids, respectively) it is a very straightforward task for the skilled man to identify peptide sequences that have, for example, at least 70% sequence identity to SEQ ID NOS: 1 and 2. Specifically, this means that for SEQ ID NO: 1 (the Gaussia luciferase signal peptide) or SEQ ID NO: 2 (the Vargula luciferase signal peptide) a derivative in accordance with claim 1 may have up to 4 amino acid residues that differ to those of SEQ ID NO: 1 or SEQ ID NO: 2. These are not large numbers of differences and so would be immediately apparent to the skilled man.

Moreover, regarding a claim drawn to a genus, "[t]he written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice, reduction to drawings, or by disclosure of relevant, identifying characteristics, i.e., structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the claimed genus. See *Eli Lilly*, 119 F.3d at 1568, 43 USPQ2d at 1406" Applicants respectfully point out that this standard has been met. Because the signal peptides were defined in the claims as being SEQ ID NO: 1 or SEQ ID NO: 2, as originally claimed and as presently amended, one of skill in the art knowing the 16 amino acid sequence of SEQ ID NO: 1 or 14 amino acids of SEQ ID NO: 2 and knowing the 20 amino acids that exist, can contemplate each and every derivative as is now claimed. Thus, it is clear that the proposed claims only permit a limited extent of variation in the specific sequences of SEQ ID NO: 1 and SEQ ID NO: 2. As a further practical restriction, Applicants describe and it is a feature of claim 1 that any derivative that may be used in the method defined therein retains the relevant functional feature of the wild type sequence, thus ensuring that only the use of functionally equivalent derivatives of SEQ ID NO: 1 and SEQ ID NO: 2 are encompassed by the claims. This functionality is easily testable and the application itself provides suitable and simple assays that may be used. Thus, the language of claim 1 merely ensures that the Applicant has coverage for sequences that are functionally equivalent and very structurally similar to SEQ ID NO: 1 or SEQ ID NO: 2, i.e. trivial modifications of these peptides that perform equivalently. This is a fair claim scope as derivative peptides that fall within the genus of signal peptides defined in claim 1 are foreseeable and it is not unduly burdensome for the skilled man to identify such peptides.

The Examiner asserts that the application does not provide a link between the structure of the genus of signal peptides defined in claim 1 and their function. On the contrary, the application shows that peptides of SEQ ID NO: 1 and peptides of SEQ ID NO: 2 are capable of driving the efficient production of a target protein in host cells. It must be remembered that these signal peptides are not merely strings of letters in a sequence listing but are molecules, albeit complex molecules, of a certain structure, that when fused to the N-terminus of other proteins, induce the highly efficient production of that protein in a host cell.

These molecules are chains of amino acid molecules and ultimately the structure of peptide molecules defined by SEQ ID NOs: 1 and 2 is dependant on those constituent amino acids. Thus, the skilled man has a reference (or starting) point in terms of structure and corresponding function and he would know from his common general knowledge that one can depart from the structure of the wild type peptides (e.g. by replacing 1, 2, 3, 4 or 5 amino acids of SEQ ID NO: 1; or 1, 2, 3 or 4 amino acids of SEQ ID NO: 2) and still obtain a signal peptide that retains the ability of SEQ ID NO: 1 or SEQ ID NO: 2 to enhance or induce secretion of the target proteins e.g. by merely replacing certain amino acids with similar amino acids, i.e. conservative substitutions.

As is hopefully clear from the foregoing, contrary to the Examiner's position, the skilled man is indeed working with a defined structure/function relationship between the molecules that are defined by SEQ ID NO: 1 and SEQ ID NO: 2 and the efficient expression of target proteins. From his common general knowledge he would be aware of how he would be able to modify these molecules by replacing certain amino acid residues with other amino acids in order to impact minimally on that structure and thereby maintain the requisite function. Thus, on the basis of the disclosure of the application as filed, the scope of the claims is foreseeable and the skilled man is readily able to work within that scope without undue experimentation and as such there is adequate written description in the application as filed.

It is further submitted that this situation is not that different to classical chemical patent claims where a new chemical entity may be defined by a chemical formula which has a defined core structure and numerous alternative options for the various side groups. It is also the case in mechanical patent applications that applicants are not required to list exhaustively the possible options for trivial features such as "fastening means". It is therefore inappropriate and unfair to apply stricter criteria to a biological case such as the present one.

Applicants file this Amendment and Response solely to facilitate prosecution. As such, Applicants reserve the right to pursue claims of broader or similar scope as originally filed in a continuation application or other application after allowance of the present application. Applicants do not concede that the current or past rejections are correct and reserve the right to challenge such rejections later in prosecution or on appeal. Accordingly, any amendment, argument, or claim cancellation is not to be construed as abandonment or

disclaimer of subject matter. Because certain of the current amendments may include broadening amendments, Applicants respectfully request the Examiner to revisit any previously reviewed references cited in this Application to further ensure that the currently pending claims remain patentable over any previously reviewed references.

Pursuant to the above remarks, reconsideration and allowance of the pending application is believed to be warranted. The Examiner is invited and encouraged to directly contact the undersigned if such contact may enhance the efficient prosecution of this application to issue.

An electronic payment in the amount of $65.00 representing the small entity fee under 37 C.F.R. 1.17(a)(1) for Request for a one (1) month Extension of Time and a Request for a one (1) month Extension of Time are submitted herewith. This amount is believed to be correct; however, the Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 14-0629.

Respectfully submitted,

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CERTIFICATE OF EFS-WEB TRANSMISSION UNDER 37 C.F.R. § 1.8

I hereby certify that this correspondence, including any items indicated as attached or included, is being transmitted by EFS-WEB on the date indicated below.

/J. Gibson Lanier, Ph.D., Reg. No. 57,519/ — April 21, 2011
J. Gibson Lanier, Ph.D. — Date